ATTACHMENT A

Marked-Up Replacement Paragraphs

Please amend the marked paragraphs in the manner and locations set forth below:

Page 24, line 24, please amend the paragraph as follows:

Further characterization of the ~19 kDa C3-binding protein was performed by fractionating 50 μl of supernatant from an overnight SA culture on a large (20 cm) 15% SDS-PAGE gel and transferring onto a PVDF membrane as described above. The membrane was subsequently stained with 0.05% Coomassie brilliant blue R250 solution for 20 min and destained with 50% methanol. Two candidate bands of interest were noted on the membrane and sent to the Protein Chemistry Laboratory (Texas A&M University, College Station, TX, USA) for N-terminal sequencing which resulted in the identification of residues S-E-G-Y-P-R-E-K-K (SEQ ID NO: 1) and F-T-F-E-P-F-P-T-N-E (SEQ ID NO: 2) corresponding to the Efb (PubMed accession number Q08691) and the SA1755 (PubMed accession number E89983) protein sequences from SA, respectively.

Page 25, line 6, please amend the paragraph as follows:

Cloning of the *sac3* and *sa1755* genes from *S. aureus* strain Newman. The *sac3* and the *sa1755* genes excluding the 5' signal sequence were amplified by polymerase chain reaction (PCR) using *S. aureus* strain Newman DNA as a template. The following oligonucleotide primers were used: 5'-CGC GGA TCC CCA AGA GAA AAG AAA CCA GTG AGT A-3' (SEQ ID NO: 3) forward primer and 5'-AAC TGC AGA GTT TTA TTT AAC TAA TCC TTG-3' (SEQ ID NO: 4) reverse primer and 5'-CGC GGA TCC CCG TTT CCT ACA AAT GAA GAA-3' (SEQ ID NO: 5) forward primer and 5'-AAC TGC AGC TAG TAT GCA TAT TCA TTA-3' (SEQ ID NO: 6) reverse primer for *sac3* and *sa1755*, respectively (IDT Inc, Coralville, IA, USA). *Bam HI* and *Pst I* restriction enzyme sites (underlined) were incorporated into the forward and reverse primers, respectively. Each reaction contained 500 ng of template DNA, 5 pmol of forward and reverse primers, 25 mM dNTPs, 1.5 mM $MgCl_2$, 16 mM $(NH_4)_2SO_4$, 67 mM Tris-HCl pH 8.8, 0.01% Tween-20, and 2 units of *Taq* DNA polymerase (CLP, San Diego, CA, USA). The reaction was

performed on a Perkin-Elmer DNA Thermocycler using the following conditions: 94°C for 1 min, 52°C for 1 min, and 72°C for 1 min for 30 cycles. The resulting PCR amplifications resulted in 400 or 351 base pair products that were subsequently TA-cloned into the pCRT7/NT-TOPO expression vector (Invitrogen, Carlsbad, CA, USA) and designated pCRT7/NT-SAC3 or pCRT7/NT-SA1755, respectively. Nucleotide sequencing was performed with the Sequenase version 2.0 sequencing kit (US Biochemicals) according to the manufacturer's instructions and by automated sequencing (Molecular Genetics Core Facility in the Department of Microbiology and Molecular Genetics, University of Texas-Houston Medical School). Sequencing of *sac3* and *sa1755* was performed using the oligonucleotide primers T7 forward 5'-TAA TAC GAC TCA CTA TAG GG-3' (SEQ ID NO: 7) and T7 reverse 5'-CTA GTT ATT GCT CAG CGG TGG -3' (SEQ ID NO: 8) (IDT Inc).

Page 38, line 23, please amend the paragraph as follows

EXPERIMENTAL PROCEDURES

Cloning of Efb Truncations from S. aureus strain Newman-The *efb* gene and *efb* truncations were amplified by polymerase chain reaction (PCR) using *S. aureus* strain Newman DNA as a template. The following oligonucleotide primers were used: 5'-CGC GGA TCC CCA AGA GAA AAG AAA CCA GTG AGT A-3' (SEQ ID NO: 3) forward primer and 5'-AAC TGC AGA GTT TTA TTT AAC TAA TCC TTG-3' (SEQ ID NO: 4) reverse primer, 5'-CGC GGA TCC CCA AGA GAA AAG AAA CCA GTG AGT A-3' (SEQ ID NO: 3) forward primer and 5'-AAC TGC AGT TAT TCT CTC ACA AGA TTT TGA GCT TG-3' (SEQ ID NO: 9) reverse primer, and 5'-CCA GCA GCG AAA ACT GAT GCA ACT-3' (SEQ ID NO: 10) forward primer and 5'-AAC TGC AGA GTT TTA TTT AAC TAA TCC TTG-3' (SEQ ID NO: 11) reverse primer for *rEfb*, *rEfb 120* and *rEfb 165*, respectively (IDT Inc., Coralville, IA, USA). The resulting PCR products were subsequently cloned using the TA Expression Kit into the pCRT7/NT-TOPO expression vector (Invitrogen, Carlsbad, CA, USA) and designated pCRT7/NT-rEfb, pCRT7/NT-rEfb120, and pCRT7/NT-rEfb165. Nucleotide sequencing of *rEfb*, *rEfb120* and *rEfb165*

were performed by automated sequencing (Molecular Genetics Core Facility, University of Texas-Houston Medical School).